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Functional Annotation of Farm Animals Initiative

FAANG Workshop
January 12, 2016

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Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project


Open Access Paper

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Why is FAANG important?

• Understanding the genotype to phenotype link
• Refining Genomic Selection for genetic improvement
• Improving fundamental understanding of biology
Goal of Workshop

• Promote information exchanges regarding recent FAANG efforts worldwide
• Provide a great forum for the FAANG community to communicate and foster the interactions and collaborations
• Provide support for next generation scientists such as graduate students and postdoctoral fellow to have opportunities to interact and gain novel knowledge and technology from peer scientists from the meeting.
• Brief introduction: Huaijun Zhou and Chris Tuggle
• Brief Introduction of RCN: Fiona McCarthy
• Progress report for each subcommittee
  – Metadata and Data Sharing Committee report: Laura Clarke
  – Animals, Samples, and Assay Committee report: Elisabetta Giuffra and Huaijun Zhou
    • DNAse-seq and ChIP-seq analysis of farm animal tissues: Pablo Ross
    • Measuring Chromatin Accessibility using ATAC-seq: preliminary results on porcine tissues/cells: Kylie Munyard
    • Functional annotation of livestock genomes using Hi-C: preliminary results on porcine tissues/cells: Herve Acloque
  – Bioinformatics and Data Analysis Committee report: James Reecy and Mick Watson
    • RNA working group: Lel Eory
    • Methylation Working group: Ole Madsen
    • Structural working group: Sylvain Foissac
    • ChIP-seq working group: Pablo Ross
• Progress report on FAANG associated projects
  – WUR-pigENCODE: Martien Groenen
  – Canada and FAANG: Graham Plastow
  – Strategy to identify regulatory mutations affecting complex traits: Ben Hayes
  – Equine FAANG: Carrie Finno
• Group discussion: Graham Plastow, Elisabetta Giuffra, Pablo Ross and Huaijun Zhou